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Proteases from Gram-Positive Organisms David A. Estell SN# Unassigned Docket No. GC381-US-D2 Sheet 1 of 11

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FIG.\_1A

Proteases from Gram-Positive Organisms David A. Estell SN# Unassigned Docket No. GC381-US-D2 Sheet 2 of 11

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610 590 ttatatgattatgaccgaaaagatgcagaaggcaagctgcgcgagctt LYDYDRKDAEGKLRE 650 630 catctgaaaaagagcattgaagtgatagaggtcccgtctattccagaa H L K K S I E V I E V P S I P E 710 690 cggcatacagttcaccatgaacaaattgaggatttgcttacaacgaca RHTVHHEQ I E D L L 750 730 ttgattgaatgcgcttacttttcggtggggaaatggaacttatcagga LIECAYFSVGKWNL 790 810 70 tcagcaagcttaaagcagcaaaaaccattccttcttatcagtgtgatt P F L L I S V I s l k Q Q K 850 830 gaaggggagggccgtatgatctctggtgagtatgtctatcctttcaaa EGEGRMISGEYVYPFK 890 910 870 aaaggagatcatatgttgctgccttacggtcttggagaatttaaactc K G D H M L L P Y G L G E F K L 930 gaaggatatgcagaatgtatcgtctcccatctg EGYAECIVS H L

FIG.\_1B

7 papa\_carpa.p vindgdvnipeyvdwrokgavtpvknogscascwafsavvtiegiikirtgnineyse OE

IYKGFTL	09	240 ?YAAKTD	:   : SLG-KTE	0	290 <sup>   </sup>	••	GT	170		ЕВНТУНН	230
soswong	50	200 210 220 230 240 YGCNGGYPWSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKTD	:  : :  :  : -EYANIHENGELG-KTE	110	280 290 <del> </del> GGIFVGPCGNKVDHA	-	KPGDFFYVPS	160 . 1	340 TSSFYPVKN	LETQQNSDTTYRLYDYDRKDAEGKLRELHLKKSIE VIEVPSIPERHTVHH	220
CWAFAAHQNG ∆	40	220 RNTYPYEGV(	: ::  : 70-vhpnd	100	(DFQLYR	- -	WDELLRRVKV	150 1	330 SNSYGVCGLY	KLRELHLKKS	210
YTIPSQRTGE	30	210 "QLVAQYGIHY	: :ILDADQDLSV	06	260 SIANQPVSVVLEAAGKDFQLYR-		SLTTMIERGEN	140 1	φγ 310 320 330 340 ILIKNSWGTGWGENGYIRKRGTGNSYGVCGLYTSSFYPVKN	YDYDRKDAEG	200
WGGTALADFG	20	200 GGYPWSAI	:  : EGDRFPLLTR	80	5 1		YGHNATTKE		¢¢ 310 ⟨NSWGTGWGE	QUSDITYRL	190
PLFFKPVFKERIWGGTALADFGYTIPSQRTGECWAFAAHQNGQSVVQNGMYKGFTL	10	190 LLDCDRRSYGCN	:  : :    :  :   :    :    :    :	70	250 RQVQPYNEGALL	••	YIIDCQKDAEIIYGHNATTKEELTTMIERGEWDELLRRVKVKPGDFFYVPSGT	120 130		:      AIGKGILALET(	180
<b>3</b> 0	ਤ ਹ	190 papa_carpa.p LLDCDRRS)	GV YJDE	MO O	250 papa_carpa.p RQVQPYNEGALLY-	<b>V</b>	YJDE	ΛΉ	300 papa_carpa.p_AVGYGPNY	YJDE	Ō <b>a</b>

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50	Ф МТТЕРLFEKPVFKERIWGGTALAD-FGYTIPSQRTGECWAFAAHQNGQSVVQNGMYKG		${\tt MTQSPIFLTPVFKEKIWGGTALRDRFGYSIPSESTGECWAISAHPKGPSTVANGPYKG}$	50	110 1	LSELWEHHRHLFGQLEGDRFPLLTKILDADQDLSVQVHPNDEYANIHENGELGKTECW		LIELWEEHREVFGGVEGDRFPLLTKLLDVKEDTSIKVHPDDYYAGENEEGELGKTECW	110 1		$^{170}$ JJ $^{1}$	V DCOKDAEIIYGHNATTKEELTTMIERGEWDELLRRVKVKPGDFFYVPSGTVHAIGKG		DCKENAEIIYGHTARSKTELVTMINSGDWEGLLRRIKIKPGDFYYVPSGTLHALCKG	170 11	
40	TGECWAFA	:: = = =	TGECWAIS		100	VQVHPNDE	<u>:</u>	IKVHPDDY	100		160	RRVKVKP	= ::	LRRIKIKPO	160	
30	-FGYTIPSQR	=======================================	RFGYSIPSES	30	06	KILDADQDLS		KLLDVKEDTS	06		150	MIERGEWDELI	- ::: ::	MINSGDWEGLI	150	FIG. 3A
20	RIWGGTALAD		KIWGGTALRD	20	80	LEGDRFPLLT	= = = = = = = = = = = = = = = = = = = =	VEGDRFPLLT	80		140	ATTKEELTTN	=======================================	ARSKTELVT	140	
10	MTTEPLFFKPVFKE	:::	MIQSPIFLTPVFKE	10	02 09	LSELWEHHRHLFGQ		LIELWEEHREVFGG	70		120 130	IDCQKDAEIIYGHN		IDCKENAEIIYGḤI	130	
	59 yjde.pep	FT	– PMI	KT	09	19 yjde.pep	IX	 PMI	Ιλ	20	ļ	79 yjde.pep	II	- PMI	AL	80

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230	SRHTVHHEQIE	i: : SYIDESTESRK	230	290	VYPFKKGDHML	=======================================	TCPLKKGDHFI	290		
220	IEVIEVPSIP	:::    : VNAATVPHVD	220	280	GEGRMISGEY		GSGLLKYEDK	280		
210	KLRELHLKKS	:     :  : SPRELHFAKA	210	270	KPFLLISVIE	:	ESFLICSVIE	270		
200	DYDRKDAEG		200	260	SGSASLKQQ	:- - - ::	INGEAEMAQD	260		: HI
80 190	$\begin{array}{c} \downarrow \downarrow \\ ALETQQNSDTTYRLYDYDRKDAEGKLRELHLKKSIEVIEVPSIPERHTVHHEQIEDLL \end{array}$	:	ቀቀ 190	0 250	TLIECAYFSVGKWNLSGSASLKQQKPFLLISVIEGEGRMISGEYVYPFKKGDHMLLPY	=======================================	<b>TFVQGEYFSVYKWDINGEAEMAQDESFLICSVIEGSGLLKYEDKTCPLKKGDHFILPA</b>	250	00 GEFKLEGYAECIVSHL	:  ::      : PDFTIKGTCTLIVSHI 310
18	39 yjde.pep			40	99 yjde.pep	GL	: PMI	W 00	30 de nen	

FIG. 38

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	IYKG	_	PLAG		<b>н</b>	TECW	=	TECW		<b>ન</b> ,	IGKG	=	LCKG	
20	NGOSAAQNGN	<u></u>	HGSSSVKNGI	50	110	NIHENGELGK'	=======================================	KLHENGDLGK	110	170 11	FYVPSGTVHA	= : : : : : : : : : : : : : : : : : : :	FYVPSGTLHA $_{\Delta\Delta}$	170
40	GECWAFAAHC	=======================================	GECWAVSAH	40	100	JOVHPNDEYA		идинерорукы	100	160	RRVKVKPGDF		RRIKIKPGDF	160
30	EPLFFKPVFKERIWGGTALAD-FGYTIPSQRTGECWAFAAHQNGQSVVQNGMYKG		HPLFLEPVFKERLWGGTKLRDAFGYAIPSQKTGECWAVSAHAHGSSSVKNGPLAG $_{\Delta}$	30	06	LSELWEHHRHLFGQLEGDRFPLLTKILDADQDLSVQVHPNDEYANIHENGELGKTECW		LDQVWKDHPEIFGFPDGKVFPLLVKLLDANMDLSVQVHPDDDYAKLHENGDLGKTECW	06	150	COKDAEIIYGHNATTKEELTTMIERGEWDELLRRVKVKPGDFFYVPSGTVHAIGKG		IDCKDDAELILGHHASTKEEFKQRIESGDWNGLLRRIKIKPGDFFYVPSGTLHALCKG $^{\Delta\Delta}$	150
20	IWGGTALAD-	_ _ _ :	<b>LWGGTKLRD</b>	20	. 80	LEGDRFPLLT		PDGKVFPLLV	80	140	ATTKEELTTM	:::::::::::::::::::::::::::::::::::::::	ASTKEEFKQR	140
10	LFEKPVFKER		LFLEPVFKER	10	70	ИЕННRHL FGQ]	= :: - ::	KOHPEI FGF!	. 70	130	KDAEIIYGHN	: : : :	DDAELILGHH	130
	MTTEP	Ξ	MTHP		09	LSELV		LDOVV	09	120	IDCOI	==	IDCK	120
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	180	190	200	210	220	230	7
39 yjde.pep	ALET(	$^{ec{\psi}\dot{\psi}}$ ALETQQNSDTTYRLYDYDRKDAEGKLRBLHLKKSIEVIEVPSIPERHTVHHEQIEDLL	DRKDAEGKLR	ELHLKKSIEV	/IEVPSIPE	кнтуннеотер	LL
TT YDHS	:   VLEIQ	:                    : : :     ::  :    :    :    : :: :	: : :    DRCNDQGQKR	:: ::   TLHIEKAME	:    : VITIPHIDK	:::: WHTPEVKEVGN	AE
II	180	44 190	200	210	220	230	
	240	250	260	270	280	290	2
99 yjde.pep	TLIE	TLIECAYFSVGKWNLSGSASLKQQKPFLLISVIEGEGRMISGEYVYPFKKGDHMLLPY	SASLKOOKPE	LLISVIEGE	GRMISGEYV	'YPFKKGDHMLI	ΡΥ
GL	••		•••	= = =	:: ::	- :	_
: YDHS	OVYVQ	VYVQSDYFSVYKWKISGRAAFPSYQTYLLGSVLSGSGRIINNGIQYECNAGSHFILPA	sraafpsyqty	TLLGSVLSGS	GRIINNGIÇ	YECNAGSHFII	PA
ы Н	240	250	260	270	280	290	-
:	300	310					
yjde.pep	GEFK 	GEFKLEGYAECIVSHL		:			
YDHS	GEFT 300	EFTIEGTCEFMISHP					

FIG.\_48

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Proteases from Gram-Positive Organisms David A. Estell SN# Unassigned Docket No. GC381-US-D2 Sheet 8 of 11

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		2	50					-	27						2
ct	gct	ggt	aaa	agct	gct	gga	cgc	caa	tat	gga	tct	ctc	cgt	gca	agtc
L	L	V	K	L	L	.D	A	N	M	D	L	S	V	Q	V
90							10						33		
ca	tcc		atga	atga	tta	tgc	aaa	act	gca	cga	aaa	tgg	cga	cct	tggt
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FIG.\_5A

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610 590 gtatacgattatgaccgctgtaatgaccagggccaaaaaagaactctt D R C N D Q G Q K R T L Y VYD 650 630 catatagaaaaagccatggaagtcataacgataccgcatatcgataaa AMEVITIPHIDK E K 710 690 gtgcatacaccggaagtaaaagaagttggtaacgctgagatcattgtt V H T P E V K E V G N A E I 750 tatgtgcaatcagattatttctcagtgtacaaatggaagattagcggc YVQSDYFSVYKWK 810 790 70 cgagctgcttttccttcatatcaaacctatttgctggggagtgttctg Q T Y L L G S V L Y RAAFPS 850 830 agcggatcaggacgaatcataaataatggtattcagtatgaatgcaat S G S G R I I N N G I Q Y E C N 910 890 870 gcaggctcacactttattctgcctgcgcattttggagaatttacaata AGSHFILPAHFGE 930 gaaggaacatgtgaattcatgatatctcatcct MISHP E G T C E F

FIG.\_5B

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FIG.\_6A

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610 590 cgggtgtacgattatgaccgtcttgatagcaacggaagtccgagagag R V Y D Y D R L D S N G S P R 670 650 630 cttcattttgccaaagcggtcaatgccgccacggttccccatgtggac AVNAATVPHVD A K 710 690 gggtatatagatgaatcgacagaatcaagaaaaggaataaccattaaa Y I DESTESRKGI 750 730 acatttgtccaaggggaatatttttcggtttataaatgggacatcaat W S V Y K F V Q G E Y F 810 790 70 ggcgaagctgaaatggctcaggatgaatcctttctgatttgcagcgtg FLICSV S M A Q D E GEAE 850 830 atagaaggaagcggtttgctcaagtatgaggacaaaacatgtccgctc D K T C P L E G S G L L K Y E 910 890 870 aaaaaaggtgatcactttattttgccggctcaaatgcccgattttacg K G D H F I L P A Q M P D 930 ataaaaggaacttgtacccttatcgtgtctcatatt KGTCTLIVSH

FIG.\_6B